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Figure 1A SEQ ID No 1.

1 GAGGTCCAGC TTCAGCAGTC TGGACCTGAC CTGGTGAAGC CTGGGGCTTC  
E V Q L Q Q S G P D L V K P G A S

51 AGTGAAGATA TCCTGCAAGG CTTCTGGTTA CTCATTCACT GGCTACTACA  
V K I S C K A S G Y S F T G Y Y

101 TGCACTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGACGT  
M H W V K Q S H G K S L E W I G R

151 ATTAATCCTA ACAATGGTGT TACTCTCTAC AACCAGAAAT TCAAGGACAA  
I N P N N G V T L Y N Q K F K D K

201 GGCCATATTA ACTGTAGACA AGTCATCCAC CACAGCCTAC ATGGAGCTCC  
A I L T V D K S S T T A Y M E L

251 GCAGCCTGAC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGATCTACT  
R S L T S E D S A V Y Y C A R S T

301 ATGATTACGA ACTATGTTAT GGACTIONG GGTCAAGTAA CCTCAGTCAC  
M I T N Y V M D Y W G Q V T S V T

351 CGTCTCCTCA GGTGGTGGTG GGAGCGGTGG TGGCGGCACT GGC GGCGGCGG  
V S S G G G G S G G G G T G G G

401 GATCTAGTAT TGTGATGACC CAGACTCCCA CATTCTGCT TGTTCAGCA  
G S S I V M T Q T P T F L L V S A

451 GGAGACAGGG TTACCATAAC CTGCAAGGCC AGTCAGAGTG TGAGTAATGA  
G D R V T I T C K A S Q S V S N D

501 TGTAGDITGG TACGAACAGA AGCGAGGGCA GTCTCCTACA CTGCTCATAT  
V A W Y Q Q K P G Q S P T L L I

551 CCTATACATC CAGTCGCTAC GCTGGAGTCC CTGATCGCTT CATTGGCAGT  
S Y T S S R Y A G V P D R F I G S

601 GGATATGGGA CGGATTTCAC TTTCACCATC AGCACTTTGC AGGCTGAAGA  
G Y G T D F T F T I S T L Q A E D

651 CCTGGCAGTT TATTTCTGTC AGCAAGATTA TAATTCTCCT CCGACGTTCC  
L A V Y F C Q Q D Y N S P P T F

701 GTGGAGGCAC CAAGCTGGAA ATCAAACGG  
G G G T K L E I K R

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Figure 1B SEQ ID No 2.

1 AAGCTTCCAC CATGGGATGG AGCTGTATCA TCCTCTTCTT GGTAGCAACA  
A S T M G W S C I I L F L V A T

51 GCTACAGGTG TCCACTCCGA GGTCCAGCTT CAGCAGTCTG GACCTGACCT  
A T G V H S E V Q L Q Q S G P D L

101 GGTGAAGCCT GGGGCTTCAG TGAAGATATC CTGCAAGGCT TCTGGTTACT  
V K P G A S V K I S C K A S G Y

151 CATTCACTGG CTACTACATG CACTGGGTGA AGCAGAGCCA TGGAAAGAGC  
S F T G Y Y M H W V K Q S H G K S

201 CTTGAGTGGA TTGGACGTAT TAATCCTAAC AATGGTGTTA CTCTCTACAA  
L E W I G R I N P N N G V T L Y N

251 CCAGAAATTC AAGGACAAGG CCATATTAAC TGTAACAAG TCATCCACCA  
Q K F K D K A I L T V D K S S T

301 CAGCCTACAT GGAGCTCCGC AGCCTGACAT CTGAGGACTC TGCGGTCTAT  
T A Y M E L R S L T S E D S A V Y

351 TACTGTGCAA GATCTACTAT GATTACGAAC TATGTTATGG ACTACTGGGG  
Y C A R S T M I T N Y V M D Y W G

401 TCAAGTAACC TCAGTCACCG TCTCCTCAGG TGGTGGTGGG AGCGGTGGTG  
Q V T S V T V S S G G G G S G G

451 GCGGCACTGG CGGCGGCGGA TCTAGTATTG TGATGACCCA GACTCCCACA  
G G T G G G G S S I V M T Q T P T

501 TTCCTGCTTG TTTCAGCAGG AGACAGGGTT ACCATAACCT GCAAGGCCAG  
F L L V S A G D R V T I T C K A S

551 TCAGAGTGTG AGTAATGATG TAGCTTGGTA CCAACAGAAG CCAGGGCAGT  
Q S V S N D V A W Y Q Q K P G Q

601 CTCCTACACT GCTCATATCC TATACATCCA GTCGCTACGC TGGAGTCCCT  
S P T L L I S Y T S S R Y A G V P

651 GATCGCTTCA TTGGCAGTGG ATATGGGACG GATTTCACTT TCACCATCAG  
D R F I G S G Y G T D F T F T I S

701 CACTTTGCAG GCTGAAGACC TGGCAGTTTA TTTCTGTCAG CAAGATTATA  
T L Q A E D L A V Y F C Q Q D Y

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751 ATTCTCCTCC GACGTTCGGT GGAGGCACCA AGCTGGAAAT CAAACGGGCC  
N S P P T F G G G T K L E I K R A

801 TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC  
S T K G P S V F P L A P S S K S T

851 CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG  
S G G T A A L G C L V K D Y F P

901 AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC  
E P V T V S W N S G A L T S G V H

951 ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT  
T F P A V L Q S S G L Y S L S S V

1001 GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG  
V T V P S S S L G T Q T Y I C N

1051 TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAAAGT TGAGCCCCAA  
V N H K P S N T K V D K K V E P K

1101 TCTTGTGACA AAACTCACAC ATGCCACCG TGCCCAGCAC CTGAACTCCT  
S C D K T H T C P P C P A P E L L

1151 GGGGGGACCG TCAGTCTTCC TCTTCCCCC AAAACCCAAG GACACCCTCA  
G G P S V F L F P P K P K D T L

1201 TGATCTCCCG GACCCCTGAG GTCACATGCG TGGTGGTGGG CGTGAGCCAC  
M I S R T P E V T C V V V D V S H

1251 GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG TGGAGGTGCA  
E D P E V K F N W Y V D G V E V H

1301 TAATGCCAAG-ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGTG  
N A K T K P R E E Q Y N S T Y R

1351 TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAG  
V V S V L T V L H Q D W L N G K E

1401 TACAAGTGCA AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TCGAGAAAC  
Y K C K V S N K A L P A P I E K T

1451 CATCTCCAAA GCCAAAGGGC AGCCCCGAGA ACCACAGGTG TACACCCTGC  
I S K A K G Q P R E P Q V Y T L

1501 CCCCATCCCG GGATGAGCTG ACCAAGAACC AGGTCAGCCT GACCTGCCTG  
P P S R D E L T K N Q V S L T C L

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1551 GTCAAAGGCT TCTATCCCAG CGACATCGCC GTGGAGTGGG AGAGCAATGG  
V K G F Y P S D I A V E W E S N G

1601 GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG  
Q P E N N Y K T T P P V L D S D

1651 GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG  
G S F F L Y S K L T V D K S R W Q

1701 CAGGGGAACG TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA  
Q G N V F S C S V M H E A L H N H

1751 CTACACGCAG AAGAGCCTCT CCCTGTCTCC GGGTAAATGA GTGCGACGGC  
Y T Q K S L S L S P G K - V R R

1801 CAAGCTT  
P S

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Figure 2. SEQ ID No3.

ATGGGCCACA CACGGAGGCA GGAACATCA CCATCCAAGT GTCCATACCT	50
M G H T R R Q G T S P S K C P Y L	
CAATTTCTTT CAGCTCTTGG TGCTGGCTGG TCTTTCTCAC TTCTGTTTCA	100
N F F Q L L V L A G L S H F C S	
GTGTTATCCA CGTGACCAAG GAAGTGAAAG AAGTGGCAAC GCTGTCCTGT	150
G V I H V T K E V K E V A T L S C	
GGTCACAATG TTTCTGTTGA AGAGCTGGCA CAAACTCGCA TCTACTGGCA	200
G H N V S V E E L A Q T R I Y W Q	
AAAGGAGAAG AAAATGGTGC TGAATATGAT GTCTGGGGAC ATGAATATAT	250
K E K K M V L T M M S G D M N I	
GGCCCGAGTA CAAGAACCGG ACCATCTTTG ATATCACTAA TAACCTCTCC	300
W P E Y K N R T I F D I T N N L S	
ATTGTGATCC TGGCTCTGCG CCCATCTGAC GAGGGCACAT ACGAGTGTGT	350
I V I L A L R P S D E G T Y E C V	
TGTTCTGAAG TATGAAAAAG ACGCTTTCAA GCGGGAACAC CTGGCTGAAG	400
V L K Y E K D A F K R E H L A E	
TGACGTTATC AGTCAAAGCT GACTTCCCTA CACCTAGTAT ATCTGACTTT	450
V T L S V K A D F P T P S I S D F	
GAAATTCCAA CTTCTAATAT TAGAAGGATA ATTTGCTCAA CCTCTGGAGG	500
E I P T S N I R R I I C S T S G G	
TTTTCCAGAG CCTCACCTCT CCTGGTTGGA AAATGGAGAA GAATTAAATG	550
F P E P H L S W L E N G E E L N	
CCATCAACAC AACAGTTTCC CAAGATCCTG AAAGTGAAGT CTATGCTGTT	600
A I N T T V S Q D P E T E L Y A V	
AGCAGCAAAC TGGATTTCAT TATGACAACC AACCACAGCT TCATGTGTCT	650
S S K L D F N M T T N H S F M C L	
CATCAAGTAT GGACATTTAA GAGTGAATCA GACCTTCAAC TGGAATACAA	700
I K Y G H L R V N Q T F N W N T	

CCAAGCAAGA GCATTTTCCT GATGGAGGCG GGGGATCCGA GGTCCAGCTT 750  
T K Q E H F P D G G G G S E V Q L

CAGCAGTCTG GACCTGACCT GGTGAAGCCT GGGGCTTCAG TGAAGATATC 800  
Q Q S G P D L V K P G A S V K I S

CTGCAAGGCT TCTGGTTACT CATTCACTGG CTACTACATG CACTGGGTGA 850  
C K A S G Y S F T G Y Y M H W V

AGCAGAGCCA TGGAAAGAGC CTTGAGTGGA TTGGACGTAT TAATCCTAAC 900  
K Q S H G K S L E W I G R I N P N

AATGGTGTTA CTCTCTACAA CCAGAAATTC AAGGACAAGG CCATATTAAC 950  
N G V T L Y N Q K F K D K A I L T

TGTAGACAAG TCATCCACCA CAGCCTACAT GGAGCTCCGC AGCCTGACAT 1000  
V D K S S T T A Y M E L R S L T

CTGAGGACTC TGCGGTCTAT TACTGTGCAA GATCTACTAT GATTACGAAC 1050  
S E D S A V Y Y C A R S T M I T N

TATGTTATGG ACTACTGGGG TCAAGTAACC TCAGTCACCG TCTCCTCAGG 1100  
Y V M D Y W G Q V T S V T V S S G

TGGTGGTGGG AGCGGTGGTG GCGGCACTGG CGGCGGCGGA TCTAGTATTG 1150  
G G G S G G G G T G G G G S S I

TGATGACCCA GACTCCCACA TTCCTGCTTG TTTCAGCAGG AGACAGGGTT 1200  
V M T Q T P T F L L V S A G D R V

ACCATAACCT GCAAGGCCAG TCAGAGTGTG AGTAATGATG TAGCTTG GTA 1250  
T I T C K A S Q S V S N D V A W Y

CCAACAGAAG CCAGGGCAGT CTCCTACACT GCTCATATCC TATACATCCA 1300  
Q Q K P G Q S P T L L I S Y T S

GTCGCTACGC TGGAGTCCCT GATCGCTTCA TTGGCAGTGG ATATGGGACG 1350  
S R Y A G V P D R F I G S G Y G T

GATTTCACTT TCACCATCAG CACTTTGCAG GCTGAAGACC TGGCAGTTTA 1400  
D F T F T I S T L Q A E D L A V Y

TTTCTGTCAG CAAGATTATA ATTCTCCTCC GACGTTCCGT GGAGGCACCA 1450  
F C Q Q D Y N S P P T F G G G T

AGCTGGAAAT CAAATAA  
K L E I K .

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Figure 3a  
B7-1.5T4.1

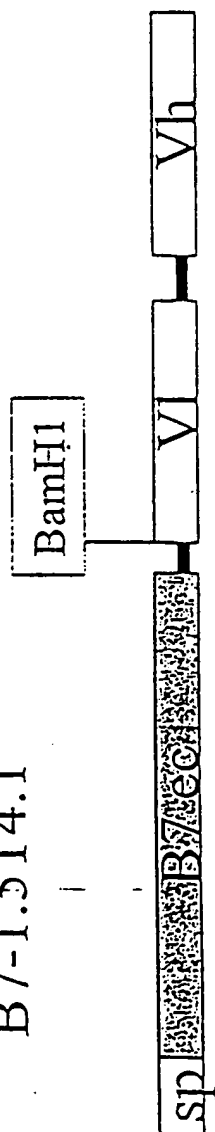
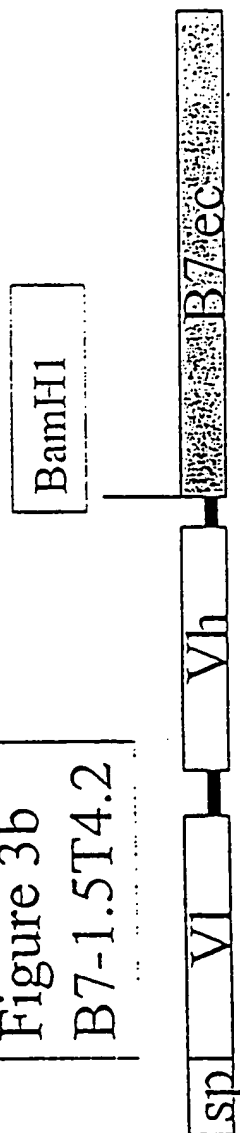


Figure 3b  
B7-1.5T4.2





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Figure 4 seq id No. 4.

Molecule Name-: B7-2(1-241)  
Sequence Printed: 1-738 (Full)  
Description:

738 bps DNA Linear  
Date Printed 02 Jun 1997

1 ATGGGACTGA GTAACATTCT CTTTGTGATG GCCTTCCTGC TCTCTGGTGC  
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51 TGCTCCTCTG AAGATTCAAG CTTATTTCAA TGAGACTGCA GACCTGCCAT  
A P L K I Q A Y F N E T A D L P

101 GCCAATTTGC AAACCTCTCAA AACCAAAGCC TGAGTGAGCT AGTAGTATTT  
C Q F A N S Q N Q S L S E L V V F

151 TGGCAGGACC AGGAAACTT GGTTCCTGAAT GAGGTATACT TAGGCAAAGA  
W Q D Q E N L V L N E V Y L G K E

201 GAAATTTGAC AGTGTTCATT CCAAGTATAT GGGCCGCACA AGTTTTGATT  
K F D S V H S K Y M G R T S F D

251 CGGACAGTTG GACCCTGAGA CTTCAACAATC TTCAGATCAA GGACAAGGGC  
S D S W T L R L H N L Q I K D K G

301 TTGTATCAAT GTATCATCCA TCACAAAAG CCCACAGGAA TGATTGCGAT  
L Y Q C I I H H K K P T G M I R I

351 CCACCAGATG AATTCTGAAC TGTCAGTGCT TGCTAACTTC AGTCAACCTG  
H Q M N S E L S V L A N F S Q P

401 AAATAGTACC AATTTCTAAT ATAACAGAAA ATGTGTACAT AAATTTGACC  
E I V P I S N I T E N V Y I N L T

451 TGCTCATCTA TACACGGTTA CCCAGAACCT AAGAAGATGA GTGTTTTGCT  
C S S I H G Y P E P K K M S V L L

501 AAGAACCAAG AATTCAACTA TCGAGTATGA TGGTATTATG CAGAAATCTC  
R T K N S T I E Y D G I M Q K S

551 AAGATAATGT CACAGAACTG TACGACGTTT CCATCAGCTT GTCTGTTTCA  
Q D N V T E L Y D V S I S L S V S

601 TTCCCTGATG TTACGAGCAA TATGACCATC TTCTGTATTC TGGAAACTGA  
F P D V T S N M T I F C I L E T D

651 CAAGACGCGG CTTTATCTT CACCTTTCTC TATAGAGCTT GAGGACCCTC  
K T R L L S S P F S I E L E D P

